(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 106 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

```
Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu Gln
 1               5                  10                  15

Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr
            20                  25                  30

Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln
        35                  40                  45

Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr
    50                  55                  60

Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg
65                  70                  75                  80

His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro
                85                  90                  95

Ile Val Lys Ser Phe Asn Arg Asn Glu Cys
            100                 105
```

SEQUENCE LISTING

B6

(1) GENERAL INFORMATION:

(i) APPLICANT: CROWE, JAMES SCOTT
LEWIS, ALAN PETER

(ii) TITLE OF INVENTION: PRODUCTION OF ANTIBODIES

(iii) NUMBER OF SEQUENCES: 46

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ
(B) STREET: 555 THIRTEENTH ST. N.W.
(C) CITY: WASHINGTON
(D) STATE: D. C.
(E) COUNTRY: U.S.
(F) ZIP: 20004

T510Y

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US 07/952640
(B) FILING DATE: 01-DEC-1992
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: ERNST, BARBARA G
(B) REGISTRATION NUMBER: 30,377
(C) REFERENCE/DOCKET NUMBER: 1808-118

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (202) 783-6040
(B) TELEFAX: (202) 783-6031

51

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GACATTCAGC TGACCCAGTC TCCA 24

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GATCAAGCTT CTAACACTCT CCCC 24

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GATCAAGCTT GACATTCAGC TGACCCAGTC TCCA 34

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

AACAGCTATG ACCATG 16

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GTTTTCCCAG TCACGAC 17

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GCGTCAGGGT GCTGCTGAGG 20

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

B4 cont'd

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGCGGGAAGA TGAAGACAGA 20

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TTCAGCAGGC ACACAACAGA 20

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1617 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

B6 Contin

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 35..92

(ix) FEATURE:
(A) NAME/KEY: mat_peptide
(B) LOCATION: 93..1465

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 35..1465

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

```
TCTAAAGAAG CCCCTGGGAG CACAGCTCAT CACC ATG GAC TGG ACC TGG AGG          52
                                      Met Asp Trp Thr Trp Arg
                                      -19             -15

TTC CTC TTT GTG GTG GCA GCA GCT ACA GGT GTC CAG TCC CAG ATG CAG       100
Phe Leu Phe Val Val Ala Ala Ala Thr Gly Val Gln Ser Gln Met Gln
            -10                 -5                  1

GTG GTG CAG TCT GGG GCT GAA GTA AAG AAG CCT GGG TCC TCG GTG ACG       148
Val Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser Ser Val Thr
      5                  10                  15

GTC TCC TGC AAG GCA TCT GGA GGC ACC TTC AGC AAC TAT GCT ATC AGC       196
Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Asn Tyr Ala Ile Ser
 20                  25                  30                  35

TGG GTG CGA CAG GCC CCT GGA CAA GGG CTT GAG TGG ATG GGA GGG ATC       244
Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Gly Ile
                 40                  45                  50

ATC CCT CTT TTT GGT ACA CCA ACC TAC TCA CAG AAC TTC CAG GGC AGA       292
Ile Pro Leu Phe Gly Thr Pro Thr Tyr Ser Gln Asn Phe Gln Gly Arg
            55                  60                  65

GTC ACG ATT ACC GCG GAC AAA TCC ACC AGC ACA GCC CAC ATG GAG CTG       340
```

```
Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala His Met Glu Leu
          70                  75                  80

ACT AGC CTG AGA TCT GAG GAC ACG GCC GTG TAT TAC TGT GCG ACA GAT      388
Thr Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Thr Asp
     85                  90                  95

CGC TAC AGG CAG GCA AAT TTT GAC CGG GCC CGG GTT GGC TGG TTC GAC      436
Arg Tyr Arg Gln Ala Asn Phe Asp Arg Ala Arg Val Gly Trp Phe Asp
100                 105                 110                 115

CCC TGG GGC CAG GGC ACC CTG GTC ACC GTC TCC TCA GCC TCC ACC AAG      484
Pro Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys
                120                 125                 130

GGC CCA TCG GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG      532
Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
            135                 140                 145

GGC ACA GCG GCC CTG GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG      580
Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
        150                 155                 160

GTG ACG GTG TCG TGG AAC TCA GGC GCC CTG ACC AGC GGC GTG CAC ACC      628
Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
    165                 170                 175

TTC CCG GCT GTC CTA CAG TCC TCA GGA CTC TAC TCC CTC AGC AGC GTG      676
Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
180                 185                 190                 195

GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG ACC TAC ATC TGC AAC      724
Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
                200                 205                 210

GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA GTT GAG CCC      772
Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro
            215                 220                 225

AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT GAA      820
Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
        230                 235                 240

CTC CTG GGG GGA CCG TCA GTC TTC CTC TTC CCC CCA AAA CCC AAG GAC      868
Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
    245                 250                 255

ACC CTC ATG ATC TCC CGG ACC CCT GAG GTC ACA TGC GTG GTG GTG GAC      916
Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
260                 265                 270                 275
```

```
GTG AGC CAC GAA GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG GAC GGC        964
Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
                280                 285                 290

GTG GAG GTG CAT AAT GCC AAG ACA AAG CCG CGG GAG GAG CAG TAC AAC       1012
Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
            295                 300                 305

AGC ACG TAC CGT GTG GTC AGC GTC CTC ACC GTC CTG CAC CAG GAC TGG       1060
Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
        310                 315                 320

CTG AAT GGC AAG GAG TAC AAG TGC AAG GTC TCC AAC AAA GCC CTC CCA       1108
Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
    325                 330                 335

GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA GGG CAG CCC CGA GAA       1156
Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
340                 345                 350                 355

CCA CAG GTG TAC ACC CTG CCC CCA TCC CGG GAT GAG CTG ACC AAG AAC       1204
Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn
                360                 365                 370

CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAT CCC AGC GAC ATC       1252
Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
            375                 380                 385

GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC       1300
Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
        390                 395                 400

ACG CCT CCC GTG CTG GAC TCC GAC GGC TCC TTC TTC CTC TAC AGC AAG       1348
Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
    405                 410                 415

CTC ACC GTG GAC AAG AGC AGG TGG CAG CAG GGG AAC GTC TTC TCA TGC       1396
Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
420                 425                 430                 435

TCC GTG ATG CAT GAG GCT CTG CAC AAC CAC TAC ACG CAG AAG AGC CTC       1444
Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
                440                 445                 450

TCC CTG TCT CCG GGT AAA TGAGTGCGAC GGCCGGCAAG CCCCCGCTCC              1492
Ser Leu Ser Pro Gly Lys
            455

CCGGGCTCTC GCGGTCGCAC GAGGATGCTT GGCACGTACC CCGTGTACAT ACTTCCCGGG     1552

CGCCCAGCAT GGAAATAAAG CACCCAGCGC TGCCCTGGGC CCCTGCGAAA AAAAAAAAAA     1612

AAAAA                                                                1617
```

B6 Canine

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 476 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

B6 Contd

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

```
Met Asp Trp Thr Trp Arg Phe Leu Phe Val Val Ala Ala Ala Thr Gly
-19                 -15                 -10                  -5

Val Gln Ser Gln Met Gln Val Val Gln Ser Gly Ala Glu Val Lys Lys
                1                   5                  10

Pro Gly Ser Ser Val Thr Val Ser Cys Lys Ala Ser Gly Gly Thr Phe
     15                  20                  25

Ser Asn Tyr Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
 30                  35                  40                  45

Glu Trp Met Gly Gly Ile Ile Pro Leu Phe Gly Thr Pro Thr Tyr Ser
                50                  55                  60

Gln Asn Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser
            65                  70                  75

Thr Ala His Met Glu Leu Thr Ser Leu Arg Ser Glu Asp Thr Ala Val
         80                  85                  90

Tyr Tyr Cys Ala Thr Asp Arg Tyr Arg Gln Ala Asn Phe Asp Arg Ala
     95                  100                 105

Arg Val Gly Trp Phe Asp Pro Trp Gly Gln Gly Thr Leu Val Thr Val
110                 115                 120                 125

Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser
                130                 135                 140

Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys
            145                 150                 155

Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu
        160                 165                 170

Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu
    175                 180                 185

Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr
190                 195                 200                 205
```

Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val
210 215 220

Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro
225 230 235

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
240 245 250

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
255 260 265

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
270 275 280 285

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
290 295 300

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
305 310 315

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
320 325 330

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
335 340 345

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
350 355 360 365

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
370 375 380

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
385 390 395

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
400 405 410

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
415 420 425

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
430 435 440 445

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
450 455

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 902 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 32..739

(ix) FEATURE:
(A) NAME/KEY: mat_peptide
(B) LOCATION: 89..739

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 32..86

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

```
CAAGAGGCAG CGCTCTCGGG ACGTCTCCAC C ATG GCC TGG GCT CTG CTG CTC          52
                                   Met Ala Trp Ala Leu Leu Leu
                                   -19             -15

CTC ACC CTC CTC ACT CAG GAC ACA GGG TCC TGG GCC CAG TCT GCC CTG        100
Leu Thr Leu Leu Thr Gln Asp Thr Gly Ser Trp Ala Gln Ser Ala Leu
        -10                 -5                  1

ACT CAG CCT GCC TCC GTG TCT GGG TCT CCT GGA CAG TCG ATC ACC ATC        148
Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln Ser Ile Thr Ile
  5                 10                  15                  20

TCC TGC ACT GGA ACC AAC AAT GAT GTT GGG AGT TAT AAC CTT GTC TCC        196
Ser Cys Thr Gly Thr Asn Asn Asp Val Gly Ser Tyr Asn Leu Val Ser
                25                  30                  35

TGG TAC CAG CAG CAC CCA GGC AAA GCC CCC AAA ATC ATG ATT TAT GAG        244
Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Ile Met Ile Tyr Glu
            40                  45                  50

GTC AGT AAG CGG CCC TCA GGG GTT TCT AAT CGC TTC TCT GGC TCC AAG        292
Val Ser Lys Arg Pro Ser Gly Val Ser Asn Arg Phe Ser Gly Ser Lys
        55                  60                  65

TCT GGC AAC ACG GCC TCC CTG ACA ATC TCT GGG CTC CAG GCT GAG GAC        340
```

```
Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu Gln Ala Glu Asp
     70                  75                  80

GAG GCT GAT TAT TAC TGC TGC TCA TAT GCA GGT AGT TAC ACT GTG GTT      388
Glu Ala Asp Tyr Tyr Cys Cys Ser Tyr Ala Gly Ser Tyr Thr Val Val
 85                  90                  95                 100

TTC GGC GGA GGG ACC AAA CTG ACC GTC CTA GGT CAG CCC AAG GCT GCC      436
Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro Lys Ala Ala
                105                 110                 115

CCC TCG GTC ACT CTG TTC CCG CCC TCC TCT GAG GAG CTT CAA GCC AAC      484
Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn
            120                 125                 130

AAG GCC ACA CTG GTG TGT CTC ATA AGT GAC TTC TAC CCG GGA GCC GTG      532
Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val
        135                 140                 145

ACA GTG GCC TGG AAG GCA GAT AGC AGC CCC GTC AAG GCG GGA GTG GAG      580
Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala Gly Val Glu
    150                 155                 160

ACC ACC ACA CCC TCC AAA CAA AGC AAC AAC AAG TAC GCG GCC AGC AGC      628
Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser Ser
165                 170                 175                 180

TAT CTG AGC CTG ACG CCT GAG CAG TGG AAG TCC CAC AGA AGC TAC AGC      676
Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg Ser Tyr Ser
                185                 190                 195

TGC CAG GTC ACG CAT GAA GGG AGC ACC GTG GAG AAG ACA GTG GCC CCT      724
Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr Val Ala Pro
            200                 205                 210

ACA GAA TGT TCA TAGGTTCTAA ACCCTCACCC CCCCCACGGG AGACTAGAGC          776
Thr Glu Cys Ser
        215

TGCAGGATCC CAGGGGAGGG GTCTCTCCTC CCACCCCAAG GCATCAAGCC CTTCTCCCTG    836

CACTCAATAA ACCCTCAATA AATATTCTCA TTGTCAATCA CAAAAAAAAA AAAAAAAAAA    896

AAAAAA                                                              902
```

B6 Continued

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 235 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

B6 Cont.

```
Met Ala Trp Ala Leu Leu Leu Thr Leu Leu Thr Gln Asp Thr Gly
-19                 -15                 -10                  -5

Ser Trp Ala Gln Ser Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser
                 1                   5                  10

Pro Gly Gln Ser Ile Thr Ile Ser Cys Thr Gly Thr Asn Asn Asp Val
     15                  20                  25

Gly Ser Tyr Asn Leu Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala
 30                  35                  40                  45

Pro Lys Ile Met Ile Tyr Glu Val Ser Lys Arg Pro Ser Gly Val Ser
                 50                  55                  60

Asn Arg Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile
             65                  70                  75

Ser Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Cys Ser Tyr
         80                  85                  90

Ala Gly Ser Tyr Thr Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val
     95                  100                 105

Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser
110                 115                 120                 125

Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser
                130                 135                 140

Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser
            145                 150                 155

Pro Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn
        160                 165                 170

Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp
    175                 180                 185

Lys Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr
190                 195                 200                 205

Val Glu Lys Thr Val Ala Pro Thr Glu Cys Ser
                210                 215
```

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 321 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

B6 Cont

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..321

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

```
GAC ATC CAG ATG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT GTA GGA        48
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
  1               5                  10                  15

GAC AGA GTC ACC ATC ACT TGC CGG GCA AGT CAG AGC ATT AGC AAT TAT        96
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Asn Tyr
            20                  25                  30

TTA AAT TGG TAT CAA CAG AAA CCA GGG AAA GCC CCT AAG CTC CTG ATC       144
Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
         35                  40                  45

TAT GCT GCA TCC AGT TTG CAA AGT GGG GTC ACA TCA AGG TTC AGT GGC       192
Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Thr Ser Arg Phe Ser Gly
     50                  55                  60

AGT GGA TCT GGG ACA GAC TTC ACT CTC ACC ATC AGC AGT CTG CAA CCT       240
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65                  70                  75                  80

GAA GAT TCT GCA ACT TAC TAC TGT CAA CAG AGT TAC AGT ACC CTG ATC       288
Glu Asp Ser Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Leu Ile
                85                  90                  95

ACC TTC GGC CAA GGG ACA CGA CTG GAG ATT AAA                           321
Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
            100                 105
```

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 107 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

```
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1               5                  10                  15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Asn Tyr
            20                  25                  30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Thr Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Ser Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Leu Ile
                85                  90                  95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
            100                 105
```

B6 Cantue

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 324 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..324

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

```
GAC ATT CAG CTG ACC CAG TCT CCA TCT TCC CTG TCT GCA TCG GTA GGA        48
Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
  1               5                  10                  15

GAC AGA GTC ACC ATC ACC TGC AGG GCA AGT CAG GGC ATT AGC GAT TAT        96
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asp Tyr
             20                  25                  30

TTA AGT TGG TAT CAG CAG AAA CCA GGG AAA GCC CCT GAG CTC CTG ATC       144
Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Glu Leu Leu Ile
         35                  40                  45

TAT GCT GCT TCC AGT TTG CAA AGT GGG ATT CCC TCT CGG TTC AGC GGC       192
Tyr Ala Ala Ser Ser Leu Gln Ser Gly Ile Pro Ser Arg Phe Ser Gly
     50                  55                  60

AGT GGA TCT GGG ACA GAT TTC ACT CTC ACC ATC AGC AGC CTG CAG CCT       240
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65                  70                  75                  80

GAA GAT TCT GCA GTT TAT TAC TGT CAA CAC ACT TAT AGT GAC CCG TAC       288
Glu Asp Ser Ala Val Tyr Tyr Cys Gln His Thr Tyr Ser Asp Pro Tyr
                 85                  90                  95

AGT TTT GGC CAG GGG ACC AAA GTG GAC ATC AAA CGA                       324
Ser Phe Gly Gln Gly Thr Lys Val Asp Ile Lys Arg
            100                 105
```

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 108 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

B6 Cont.

```
Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1               5                  10                  15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asp Tyr
            20                  25                  30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Glu Leu Leu Ile
        35                  40                  45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Ile Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Ser Ala Val Tyr Tyr Cys Gln His Thr Tyr Ser Asp Pro Tyr
                85                  90                  95

Ser Phe Gly Gln Gly Thr Lys Val Asp Ile Lys Arg
            100                 105
```

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 324 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

B6 Cont'd

(iv) ANTI-SENSE: NO

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..324

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

```
GAC ATT CAG CTG ACC CAG TCT CCA TCC TCC CTG TCT GCT TCT GTA GGA        48
Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
  1               5                  10                  15

GAC AGA GTC ACC ATC ACT TGC CGG GCA AGT CAG GGC ATT AGC ACT TAT        96
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Thr Tyr
             20                  25                  30

TTA AGT TGG TAT CAG CAG AAA CCA GGG AAA GCC CCT AAG CTC CTG ATC       144
Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
         35                  40                  45

TAT TAT GCA AAC AGT TTG GCA AGT GGG GTC CCA TCA AGG TTC AGC GGC       192
Tyr Tyr Ala Asn Ser Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly
     50                  55                  60

AGT GGA TCT GGG ACA GAA TTC ACT CTC ACC ATC AGC AGC CTG CAG CCT       240
Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65                  70                  75                  80

GAA GAT TCT GCA ACT TAT TAC TGT GGA CAG GGT AAT AGT TAC CCT CTC       288
Glu Asp Ser Ala Thr Tyr Tyr Cys Gly Gln Gly Asn Ser Tyr Pro Leu
                 85                  90                  95

ACT TTC GGC GGA GGG ACC AAG GTG GAG ATC AAA CGA                       324
Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
            100                 105
```

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 108 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

```
Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1               5                  10                  15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Thr Tyr
            20                  25                  30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45

Tyr Tyr Ala Asn Ser Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Ser Ala Thr Tyr Tyr Cys Gly Gln Gly Asn Ser Tyr Pro Leu
                85                  90                  95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
            100                 105
```

B6 Cont'd

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 324 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..324

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

```
GAC ATT CAG CTG ACC CAG TCT CCA TCC TCT CAG TCT GCA TCT GTA GGA        48
Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Gln Ser Ala Ser Val Gly
  1               5                  10                  15

GAC AGA GTG ACC ATT ACT TGC CAG GCG AGT CAA AGC CTT AGC AAT TAT        96
Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Ser Leu Ser Asn Tyr
            20                  25                  30

TTA AAT TGG TAT CAG CAG AAA CCA GGG AAA ATT CCT AAG CTC CTG ATC       144
Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ile Pro Lys Leu Leu Ile
        35                  40                  45

TAT AGG GCA TCC AGT TTG CAA AGT GGG ATT CCC TCT CGG TTC AGC GGC       192
Tyr Arg Ala Ser Ser Leu Gln Ser Gly Ile Pro Ser Arg Phe Ser Gly
    50                  55                  60

AGT GGA TCT GGG ACG GAT TTC ACT CTC ACC ATC AGC AGC CTG CAG CCT       240
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

GAA GAT TTT GCC ACT TAT TAC TGT CAG CAT AAT TAT GGT ACC CCT CTC       288
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Asn Tyr Gly Thr Pro Leu
                85                  90                  95

ACT TTC GGC GGA GGG ACC AAG GTG GAG ATC AAA CGA                       324
Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
            100                 105
```

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 108 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

b6 Canc

```
Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Gln Ser Ala Ser Val Gly
 1               5                  10                  15

Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Ser Leu Ser Asn Tyr
            20                  25                  30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ile Pro Lys Leu Leu Ile
        35                  40                  45

Tyr Arg Ala Ser Ser Leu Gln Ser Gly Ile Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Asn Tyr Gly Thr Pro Leu
                85                  90                  95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
            100                 105
```

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 324 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..324

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GACATTCAGC TGACCCAGTC TCCACTCTCC CTGCCCGTCA GTCTTGGAGA GTCGGCCTCC 60

ATCTCCTNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN 120

NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNTCCCAGAC 180

AGGTTCACTG GCAGTGGGTC AGGCACTGAT TTCACACTGA AAATCAGCAG AGTGGAGGCT 240

GAGGATGTTG GGGTTTATTA CTGCATGCAA GCTCTTCGGT CTCCTTGGAC GTTCGGCCAA 300

GGGACCAAGG TGGAAATCAG ACGA 324

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 108 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Asp Ile Gln Leu Thr Gln Ser Pro Leu Ser Leu Pro Val Ser Leu Gly
1 5 10 15

Glu Ser Ala Ser Ile Thr Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
20 25 30

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
35 40 45

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Pro Asp Arg Phe Thr Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala
65 70 75 80

Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala Leu Arg Ser Pro Trp
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Arg Arg
100 105

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 108 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Asp Ile Gln Leu Thr Gln Ser Pro Leu Ser Leu Pro Val Ser Leu Gly
1 5 10 15

Glu Ser Ala Ser Ile Thr Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
20 25 30

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
35 40 45

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Pro Asp Xaa Xaa Thr Xaa
50 55 60

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Lys Xaa Xaa Arg Val Glu Ala
65 70 75 80

Xaa Xaa Val Gly Val Xaa Xaa Xaa Met Xaa Ala Leu Arg Ser Pro Trp
85 90 95

Xaa Xaa Xaa Xaa Xaa Xaa Lys Val Xaa Xaa Arg Arg
100 105

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 324 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..324

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

```
GAC ATT CAG CTG ACC CAG TCT CCA TCT TCC CTG TCT GCA TCG GTA GGA        48
Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
  1               5                  10                  15

GAC AGA GTC ACC ATC ACC TGC AGG GCA AGT CAG GGC ATT AGC GAT TAT        96
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asp Tyr
             20                  25                  30

TTA AGT TGG TAT CAG CAG AAA CCA GGA AAA GCT CCT AAG CTC CTG ATC       144
Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
         35                  40                  45

TAT GCT GCA TCC AGT TTG CAA AGT GGG GTC CCA TCA AGG TTC AGC GGC       192
Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
     50                  55                  60

AGT GGA TCT GGG ACA GAA TTC ACT CTC ACC ATC AGC AGC CTG CAA CCT       240
Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65                  70                  75                  80

GAA GAT TTT GCA ACT TAT TAC TGT CTA CAG GGT TAT GGT ACC CCG TAC       288
Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln Gly Tyr Gly Thr Pro Tyr
                 85                  90                  95

AGT TTT GGC CAG GGG ACC AAA GTG GAG ATC AAA CGA                       324
Ser Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105
```

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 108 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

```
Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1               5                  10                  15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asp Tyr
            20                  25                  30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln Gly Tyr Gly Thr Pro Tyr
                85                  90                  95

Ser Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105
```

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 324 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..324

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

```
GAC ATT CAG CTG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT GTG GGA        48
Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
  1               5                  10                  15

GAC ACA GTC ACC ATC ACT TGT CGG GCA AGT CAG GAC ATT AGC AAT AAT        96
Asp Thr Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Ser Asn Asn
            20                  25                  30

TTA GTC TGG TAT CAG CAG AAA CCA GGG AAA GCC CCT AAG CTC CTG ATC       144
Leu Val Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45

TAT GCT GCA TCC AGA TTG CAA GAT GGG GTC CCA TCA AGG TTC AGC GGC       192
Tyr Ala Ala Ser Arg Leu Gln Asp Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

AGT GGG TCT GGG ACC GAT TTC ACC CTC ACA ATT AAT CCT GTG GAA GCT       240
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Pro Val Glu Ala
65                  70                  75                  80

GAC GAT GCT GCG GAT TAC TAC TGT CTA CAG ACT AAG AGT TCT CCT CGG       288
Asp Asp Ala Ala Asp Tyr Tyr Cys Leu Gln Thr Lys Ser Ser Pro Arg
                85                  90                  95

ACG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA CGA                       324
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105
```

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 108 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

```
Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1               5                  10                  15

Asp Thr Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Ser Asn Asn
            20                  25                  30

Leu Val Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45

Tyr Ala Ala Ser Arg Leu Gln Asp Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Pro Val Glu Ala
65                  70                  75                  80

Asp Asp Ala Ala Asp Tyr Tyr Cys Leu Gln Thr Lys Ser Ser Pro Arg
                85                  90                  95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105
```